

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/063,778

DATE: 07/16/98
TIME: 10:44:59

INPUT SET: S27489.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANTS: ARIYASU, Toshio
6 NAKAMURA, Shuji
7 ORITA, Kunzo
8
9 (ii) TITLE OF INVENTION: HEDGEHOG PROTEIN
10
11 (iii) NUMBER OF SEQUENCES: 31
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: BROWDY AND NEIMARK
15 (B) STREET: 419 Seventh Street N.W., Ste. 300
16 (C) CITY: Washington
17 (D) STATE: D.C.
18 (E) COUNTRY: United States of America
19 (F) ZIP: 20004
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 09/063,778
29 (B) FILING DATE: 22-APR-1998
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: JP 97-121578
33 (B) FILING DATE: 25-APR-1997
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: JP 98-
37 (B) FILING DATE: 14-APR-1998
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Browdy, Roger L.
41 (B) REGISTRATION NUMBER: 25,618
42 (C) REFERENCE/DOCKET NUMBER: ARIYASU=1
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (202) 628-5197
46 (B) TELEFAX: (202) 737-35281

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47
48 (2) INFORMATION FOR SEQ ID NO: 1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 176 amino acids
52 (B) TYPE: amino acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: protein
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
58
59 Cys Gly Pro Gly Arg Gly Pro Val Gly Arg Arg Arg Tyr Ala Arg Lys
60 1 5 10 15
61
62 Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe Val Pro Gly Val Pro Glu
63 20 25 30
64
65 Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu Gly Arg Val Ala Arg Gly
66 35 40 45
67
68 Ser Glu Arg Phe Arg Asp Leu Val Pro Asn Tyr Asn Pro Asp Ile Ile
69 50 55 60
70
71 Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp Arg Leu Met Thr Glu Arg
72 65 70 75 80
73
74 Cys Lys Glu Arg Val Asn Ala Leu Ala Ile Ala Val Met Asn Met Trp
75 85 90 95
76
77 Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His
78 100 105 110
79
80 His Ala Gln Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile Thr
81 115 120 125
82
83 Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala
84 130 135 140
85
86 Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Arg Asn His Ile
87 145 150 155 160
88
89 His Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly
90 165 170 175
91
92 (2) INFORMATION FOR SEQ ID NO: 2:
93
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 374 amino acids
96 (B) TYPE: amino acid
97 (C) STRANDEDNESS: single
98 (D) TOPOLOGY: linear
99

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100      (ii) MOLECULE TYPE: protein
101
102      (ix) FEATURE:
103          (A) NAME/KEY: mat peptide
104          (B) LOCATION: 1..176
105          (C) IDENTIFICATION METHOD: S
106
107      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
108
109      Cys Gly Pro Gly Arg Gly Pro Val Gly Arg Arg Arg Tyr Ala Arg Lys
110          1          5          10          15
111
112      Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe Val Pro Gly Val Pro Glu
113          20          25          30
114
115      Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu Gly Arg Val Ala Arg Gly
116          35          40          45
117
118      Ser Glu Arg Phe Arg Asp Leu Val Pro Asn Tyr Asn Pro Asp Ile Ile
119          50          55          60
120
121      Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp Arg Leu Met Thr Glu Arg
122          65          70          75          80
123
124      Cys Lys Glu Arg Val Asn Ala Leu Ala Ile Ala Val Met Asn Met Trp
125          85          90          95
126
127      Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His
128          100          105          110
129
130      His Ala Gln Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile Thr
131          115          120          125
132
133      Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala
134          130          135          140
135
136      Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Arg Asn His Ile
137          145          150          155          160
138
139      His Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly
140          165          170          175
141
142      Cys Phe Pro Gly Asn Ala Thr Val Arg Leu Trp Ser Gly Glu Arg Lys
143          180          185          190
144
145      Gly Leu Arg Glu Leu His Arg Gly Asp Trp Val Leu Thr Ala Asp Ala
146          195          200          205
147
148      Ser Gly Arg Val Val Pro Thr Pro Val Leu Leu Phe Leu Asp Arg Asp
149          210          215          220
150
151      Leu Gln Arg Arg Ala Ser Phe Val Ala Val Glu Thr Glu Trp Pro Pro
152          225          230          235          240

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153
154 Arg Lys Leu Leu Leu Thr Pro Trp His Leu Val Phe Ala Ala Arg Gly
155 245 250 255
156
157 Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro Val Phe Ala Arg Arg Leu
158 260 265 270
159
160 Arg Ala Gly Asp Ser Val Leu Ala Pro Gly Gly Asp Ala Leu Arg Pro
161 275 280 285
162
163 Ala Arg Val Ala Arg Val Ala Arg Glu Glu Ala Val Gly Val Phe Ala
164 290 295 300
165
166 Pro Leu Thr Ala His Gly Thr Leu Leu Val Asn Asp Val Leu Ala Ser
167 305 310 315 320
168
169 Cys Tyr Ala Val Leu Glu Ser His Gln Trp Ala His Arg Ala Phe Ala
170 325 330 335
171
172 Pro Leu Arg Leu Leu His Ala Leu Gly Ala Leu Leu Pro Gly Gly Ala
173 340 345 350
174
175 Val Gln Pro Thr Gly Met His Trp Tyr Ser Arg Leu Leu Tyr Arg Leu
176 355 360 365
177
178 Ala Glu Glu Leu Leu Gly
179 370
180

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 184 (A) LENGTH: 396 amino acids
185 (B) TYPE: amino acid
186 (C) STRANDEDNESS: single
187 (D) TOPOLOGY: linear
188

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- 192 (A) NAME/KEY: sig peptide
193 (B) LOCATION: -22..-1
194 (C) IDENTIFICATION METHOD: S
195 (A) NAME/KEY: mat peptide
196 (B) LOCATION: 1..176
197 (C) IDENTIFICATION METHOD: S
198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

200
201 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
202 -20 -15 -10
203
204 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
205 -5 1 5 10

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206
207 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
208           15                      20                      25
209
210 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
211           30                      35                      40
212
213 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
214           45                      50                      55
215
216 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
217           60                      65                      70
218
219 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
220           75                      80                      85                      90
221
222 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
223           95                      100                     105
224
225 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
226           110                     115                     120
227
228 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
229           125                     130                     135
230
231 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
232           140                     145                     150
233
234 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
235           155                     160                     165                     170
236
237 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
238           175                     180                     185
239
240 Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
241           190                     195                     200
242
243 Val Leu Thr Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
244           205                     210                     215
245
246 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
247           220                     225                     230
248
249 Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
250           235                     240                     245                     250
251
252 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
253           255                     260                     265
254
255 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
256           270                     275                     280
257
258 Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu

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SEQUENCE VERIFICATION REPORT
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Original Text